

10/659,747

=> d his

(FILE 'HOME' ENTERED AT 11:35:31 ON 12 JUL 2005)

FILE 'REGISTRY' ENTERED AT 11:35:39 ON 12 JUL 2005  
L1 SCREEN 1839 AND 1994  
L2 STRUCTURE UPLOADED  
L3 QUE L2 AND L1  
L4 50 S L3

FILE 'STNGUIDE' ENTERED AT 11:36:10 ON 12 JUL 2005

FILE 'REGISTRY' ENTERED AT 11:37:58 ON 12 JUL 2005  
L5 15075 S L3 FULL

FILE 'STNGUIDE' ENTERED AT 11:40:21 ON 12 JUL 2005

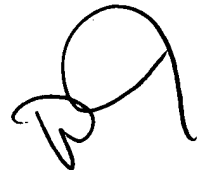
FILE 'REGISTRY' ENTERED AT 11:41:14 ON 12 JUL 2005  
L6 SCREEN 2039 AND 1839 AND 1994  
L7 STRUCTURE UPLOADED  
L8 QUE L7 AND L6  
L9 2 S L8  
L10 50 S L8 FULL

FILE 'CAPLUS' ENTERED AT 11:41:40 ON 12 JUL 2005  
L11 15 S L10

FILE 'STNGUIDE' ENTERED AT 11:42:46 ON 12 JUL 2005

FILE 'REGISTRY' ENTERED AT 11:44:15 ON 12 JUL 2005  
L12 ANALYZE L10 1- LC : 6 TERMS

=> log y

A handwritten mark, possibly a signature or initials, consisting of a large loop and a trailing stroke.

10/659,747

ENTER SCREEN EXPRESSION OR (END):end

=> screen 2039 AND 1839 AND 1994

L6 . SCREEN CREATED

=>

Uploading C:\Program Files\Stnexp\Queries\10659747b.str

L7 STRUCTURE UPLOADED

=> que L7 AND L6

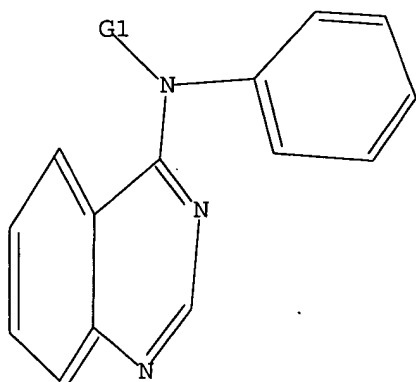
L8 QUE L7 AND L6

=> d

L8 HAS NO ANSWERS

L6 SCR 2039 AND 1839 AND 1994

L7 STR



G1 H,Ak

Structure attributes must be viewed using STN Express query preparation.

L8 QUE ABB=ON PLU=ON L7 AND L6

=> s l8

SAMPLE SEARCH INITIATED 11:41:29 FILE 'REGISTRY'

SAMPLE SCREEN SEARCH COMPLETED - 2 TO ITERATE

100.0% PROCESSED 2 ITERATIONS

2 ANSWERS

SEARCH TIME: 00.00.01

FULL FILE PROJECTIONS: ONLINE \*\*COMPLETE\*\*  
BATCH \*\*COMPLETE\*\*

PROJECTED ITERATIONS: 2 TO 124

PROJECTED ANSWERS: 2 TO 124

L9 2 SEA SSS SAM L7 AND L6

=> s l8 full

FULL SEARCH INITIATED 11:41:34 FILE 'REGISTRY'

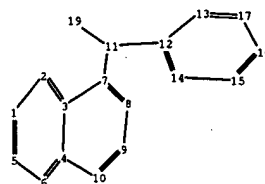
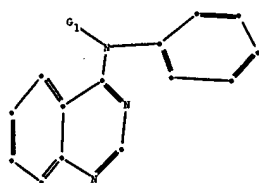
FULL SCREEN SEARCH COMPLETED - 52 TO ITERATE

10/659,747

100.0% PROCESSED      52 ITERATIONS  
SEARCH TIME: 00.00.01

50 ANSWERS

L10      50 SEA SSS FUL L7 AND L6



chain nodes :

11 19

ring nodes :

1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17

chain bonds :

7-11 11-12 11-19

ring bonds :

1-2 1-5 2-3 3-4 3-7 4-6 4-10 5-6 7-8 8-9 9-10 12-13 12-14 13-17 14-15  
15-16 16-17

exact/norm bonds :

7-11 11-12 11-19

normalized bonds :

1-2 1-5 2-3 3-4 3-7 4-6 4-10 5-6 7-8 8-9 9-10 12-13 12-14 13-17 14-15  
15-16 16-17

G1:H,Ak

Match level :

1:Atom 2:Atom 3:Atom 4:Atom 5:Atom 6:Atom 7:Atom 8:Atom 9:Atom 10:Atom 11:CLASS  
12:Atom 13:Atom 14:Atom 15:Atom 16:Atom 17:Atom 19:CLASS